AMENDMENTS

Amendments to the claims:

Please cancel claims 46-63, 66-69, 72-78, 80, 81, and 84-91 without prejudice or disclaimer, and please amend claims 64, 65, 71, 79, and 82 as set forth in the complete listing of the claims that follows. This complete listing of the claims replaces previous claim listings.

1-63. (Cancelled)

64. (Currently amended) ~~The method according to claim 63~~ An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

compress the intermediate data set, the intermediate data set having a plurality of data values associated with respective points in an array of data;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein a compressed data value is a real number that includes a whole portion representing the difference between two points in an array of data.

65. (Currently amended) ~~The method according to claim 63~~ An automated

method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

compress the intermediate data set, the intermediate data set having a plurality of data values associated with respective points in an array of data;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein a compressed data value is a real number that includes a decimal portion representing the difference between a maximum value of all the data values and a value at a particular point in an array.

66-69. (Cancelled)

70. (Previously presented) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set; the residual baseline is derived from data remaining in the intermediate data set after the areas around the putative peaks have been removed; and

wherein an area equal to twice the width of the Gaussian is removed from the left of the center line of the putative peaks.

71. (Currently amended) ~~The method according to claim 69,~~ An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set, wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set and the residual baseline is derived from data remaining in the intermediate data set after the areas around the putative peaks have been removed ;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein an area equivalent to 50 daltons is removed from the right of the center line of the putative peaks.

72-78. (Cancelled)

79. (Currently amended) ~~The~~ An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein the identifying step includes deriving a peak probability for the putative peak, and wherein peak probability is derived by using an allelic ratio, the allelic ratio being a comparison of two peak heights indicated in the corrected data.

80-81. (Cancelled)

82. (Currently amended) ~~The method according to claim 81~~ An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;
correct a baseline from the denoised data to generate an intermediate data set;
define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;
generate a residual baseline by removing the putative peaks from the intermediate data set;
remove the residual baseline from the intermediate data set to generate a corrected data set;
locate a putative peak in the corrected data set; and
identify the component that corresponds to the located putative peak;

wherein the identifying step includes calculating a peak probability that a putative peak in the corrected data is a peak indicating composition of the DNA sample; and

wherein peak probability is calculated for each of a plurality of putative peaks in the corrected data and a highest probability is compared to a second-highest probability to generate a calling ratio.

83. (Previously presented) The method according to claim 82 wherein the calling ratio is used to determine if the composition of the DNA sample will be called.

84-91. (Cancelled)